Application No.: 10/561,877 6 Docket No.: 61506(71699)

## AMENDMENTS TO THE CLAIMS

(Currently Amended) A method for diagnosing cancer, comprising the
detection of a methylated SPARC nucleic acid molecule or a variant thereof in a sample
from a subject, wherein the methylated SPARC nucleic acid molecule comprises a
sequence corresponding to the nucleic acid sequence set forth in SEQ ID NO: 1 (Figure
6).

- (Original) The method of claim 1 wherein the presence of a methylated
   SPARC nucleic acid molecule is compared to a sample from a subject without cancer.
- (Original) The method of claim 1 wherein the sample is obtained from a mammal suspected of having a proliferative cell growth disorder.
- (Original) The method of claim 1 wherein the sample is obtained from a mammal suspected of having a pancreatic cancer.
- 5. (Cancelled)
- (Previously Presented) The method of claim 1, wherein a methylated SPARC nucleic acid molecule comprises a sequence having at least about 80% sequence identity to a molecule identified in SEQ ID NO: 1 (Figure 6).
- (Previously Presented) The method of claim 1, wherein a methylated SPARC nucleic acid molecule comprises a sequence having at least about 90% sequence identity to a molecule identified in SEQ ID NO: 1 (Figure 6).
- (Previously Presented) The method of claim 1, wherein a methylated SPARC nucleic acid molecule comprises a sequence having at least about 95% sequence identity to a molecule identified in SEQ ID NO: 1 (Figure 6).

(Currently Amended) The method of claim 1, wherein the nucleic acid
molecule is expressed at least <u>at</u> a lower level in a patient with cancer as compared to
expression levels in a normal individual.

- 10. (Previously Presented) The method of claim 1, wherein the nucleic acid molecule is expressed at least about 5 fold lower in a patient with cancer as compared to expression in a normal individual.
- 11. (Previously Presented) The method of claim 1, wherein the nucleic acid molecule is expressed at least about 10 fold lower in a patient with cancer as compared to expression in a normal individual.
- 12. (Previously Presented) The method of claim 1 wherein the cancer is a pancreatic cancer.
- 13. (Previously Presented) The method of claim 1 wherein the subject sample is obtained from a mammalian patient.
- 14. (Previously Presented) The method of claim 1 wherein the subject sample is obtained from a human patient.
- (Cancelled)
- (Cancelled)
- (Previously Presented) A method of claim 1 wherein the method of detecting a methylated SPARC nucleic acid comprising methylation specific polymerase chain reaction (MSP).
- 18. (Original) A method for detecting a methylated CpG-containing SPARC nucleic acid molecule comprising: contacting a nucleic acid-containing specimen with bisulfite to modify unmethylated cytosine to uracil; contacting the SPARC nucleic acid

molecule with oligonucleotide primers that discriminate between methylated and unmethylated CpGs; and detecting the methylated CpGs in the nucleic acid.

- (Original) The method of claim 18, further comprising amplifying the CpGcontaining nucleic acid in the specimen by means of the oligonucleotide primers.
- 20. (Original) The method of claim 19, wherein the amplifying step is the polymerase chain reaction (PCR).
- 21. (Original) The method of claim 18, wherein the CpG-containing nucleic acid is in a promoter region.
- 22. (Original) The method of claim 21, wherein the promoter is a tumor suppressor gene promoter.
- 23. (Original) The method of claim 18, wherein the specimen is from a tissue selected from the group consisting of pancreas, brain, colon, urogenital, lung, renal, hematopoietic, breast, thymus, testis, ovarian, and uterine.
- 24. (New) A method for diagnosing cancer, comprising the detection of a methylated SPARC nucleic acid molecule or a variant thereof in a sample from a subject, wherein the nucleic acid molecule is expressed at least about 5 fold lower in a patient with cancer as compared to expression in a normal individual.